

LOCUS BG529820 826 bp mRNA linear EST 03-APR-2001  
 DEFINITION 602558904F1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4696752 5',  
 mRNA sequence.  
 ACCESSION BG529820  
 VERSION BG529820.1 GI:13521357  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 826)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM1524 row: h column: 01  
 High quality sequence stop: 820.

FEATURES Location/Qualifiers  
 source 1..826  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4696752"  
 /tissue\_type="embryonal carcinoma"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_61"  
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1:  
 SfiI (ggccgcctcggcc); Site\_2: SfiI (ggccattatggcc);  
 Double-stranded cDNA was prepared from cell line RNA. 5'  
 and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor  
 sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'  
 (where B = A, C, or G and N = A, C, G, or T). Average  
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC  
 Library."

# ORIGIN

Query Match 44.8%; Score 733.6; DB 12; Length 826;  
 Best Local Similarity 97.6%; Pred. No. 3.5e-161;  
 Matches 798; Conservative 0; Mismatches 14; Indels 6; Gaps 5;

Qy 1 GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCT 60  
 |||||  
 Db 11 GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCT 70  
 Qy 61 GACACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGC 120

Db	71		GACACCTGGGAAGATGGCCGGCCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGC	130
Qy	121		CACCTTGATCCAAGCCACCCCTCAGTCCCCTGAGTTCTCATCCTCGGCCCAAAGTCAT	180
Db	131		CACCTTGATCCAAGCCACCCCTCAGTCCCCTGAGTTCTCATCCTCGGCCCAAAGTCAT	190
Qy	181		CAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCT	240
Db	191		CAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCT	250
Qy	241		GCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT	300
Db	251		GCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT	310
Qy	301		GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCA	360
Db	311		GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCA	370
Qy	361		GCTGCAGGTGAAGCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACAT	420
Db	371		GCTGCAGGTGAAGCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACAT	430
Qy	421		GGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGA	480
Db	431		GGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGA	490
Qy	481		GGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCCCTCAG	540
Db	491		GGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCCCTCAG	550
Qy	541		TGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTATAAGCTCTCCTTCCT	600
Db	551		TGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTATAAGCTCTCCTTCCT	610
Qy	601		GGTGAACGCCTT-AGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGCCCAATCTAG	659
Db	611		GGTGAACGCCTTAAAGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGCCCAATCTAG	670
Qy	660		TGAAAAACCAGCTGTGTCCC--GTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCT	717
Db	671		TGAAAAACCAGCTGTGTCCCCGTGAATCGAGGCTTCCTTCAATGGCATGTATGCAGACCT	730
Qy	718		-CCTGCAGCTGGTGAAGGTGCCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTC	776
Db	731		CCCTGCAGCTGGTGAAGGTGCCATTTTCCCTCAGCATTGACCG-CTGGAGTTGGACCTTC	789
Qy	777		TGTATCCTGCCATCAAGGGTGACACCATTGAGCTCTAC	814
Db	790		TTGTATCTGCCATC-AGGGTGACCCCATTCAGTTCTAC	826